

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/763,712

DATE: 03/07/2001
 TIME: 13:13:29

Input Set : A:\37157SEQ.txt
 Output Set: N:\CRF3\03072001\I763712.raw

ENTERED

Francine

3 <110> APPLICANT: Wakamiya, N.
 5 <120> TITLE OF INVENTION: Novel Collectin
 7 <130> FILE REFERENCE: 19036/37157
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/763,712
 C--> 9 <141> CURRENT FILING DATE: 2001-02-26
 9 <150> PRIOR APPLICATION NUMBER: JP HEI 10-237611
 10 <151> PRIOR FILING DATE: 1998-08-24
 12 <160> NUMBER OF SEQ ID NOS: 32
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 2024
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo Sapiens
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (670)..(1695)
 23 <400> SEQUENCE: 1

24	gtcacgaate	tcagcaaga	taccagcgtg	ctccagggca	atctgcagaa	ccaaatgtat	60
25	tctcataatg	tggatcatat	gaacctcaac	aacctgaacc	tgacctcagg	gcagcagagg	120
26	aacctcatca	cgaatctgca	gcggtctgtg	gatgacacaa	gccagcgtat	ccagcgaatc	180
27	aagaacgact	ttcaaaatct	gcagcaggtt	tttcttcaag	ccaagaagga	cacggattgg	240
28	ctgaaggaga	aagtgcagag	cttgacagacg	ctggctgcca	acaactctgc	gttggccaaa	300
29	gccaacaacg	acaccttgga	ggatatgaac	agccagctca	actcattcac	aggtcagatg	360
30	yagaacatca	ccactatctc	tcaagccaac	gagcagaacc	tgaaagacct	gcaggactta	420
31	cacaaagatg	cagagaatag	aacagccatc	aagttcaacc	aactggagga	acgcttccag	480
32	ctctttgaga	cggatatgtt	gaacatcatt	agcaatatca	gttacacagc	ccaccacctg	540
33	cggacgctga	ccagcaatct	aatgaagtc	aggaccactt	gcacagatac	ccttaccaaa	600
34	cacacagatg	atctgacctc	cttgaataat	accctggcca	acatccgttt	ggattctgtt	660
35	tctctcagg	atg caa caa	gat ttg atg	agg tct agg	tta gac act	gaa gta	711
36	Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val						
37	1	5	10				
38	gcc aac tta	tca gtg att	atg gaa gaa	atg aag cta	gta gac tcc	aag	759
39	Ala Asn Leu	Ser Val Ile	Met Glu Glu	Met Lys Leu	Val Asp Ser	Lys	
40	15	20	25	30			
41	cat ggt cag	ctc atc aag	aat ttt aca	ata cta caa	ggt cca ccg	ggc	807
42	His Gly Gln	Leu Ile Lys	Asn Phe Thr	Ile Leu Gln	Gly Pro Pro	Gly	
43	35	40	45				
44	ccc agg ggt	cca aga ggt	gac aga gga	tcc cag gga	ccc cct ggc	cca	855
45	Pro Arg Gly	Pro Arg Gly	Asp Arg Gly	Ser Gln Gly	Pro Pro Gly	Pro	
46	50	55	60				
47	act ggc aac	aag gga cag	aaa gga gag	aag ggg gag	cct gga cca	cct	903
48	Thr Gly Asn	Lys Gly Gln	Lys Gly Glu	Lys Gly Glu	Pro Gly Pro	Pro	
49	65	70	75				
50	ggc cct gcg	ggt gag aga	ggc cca att	gga cca gct	ggt ccc ccc	gga	951
51	Gly Pro Ala	Gly Glu Arg	Gly Pro Ile	Gly Pro Ala	Gly Pro Pro	Gly	
52	80	85	90				
53	gag cgt ggc	ggc aaa gga	tct aaa ggc	tcc cag ggc	ccc aaa ggc	tcc	999
54	Glu Arg Gly	Gly Lys Gly	Ser Lys Gly	Ser Gln Gly	Pro Lys Gly	Ser	

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55 95          100          105          110
56 cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca 1047
57 Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro
58          115          120          125
59 ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc 1095
60 Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly
61          130          135          140
62 cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg 1143
63 Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val
64          145          150          155
65 cct gga cct ccg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca 1191
66 Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro
67          160          165          170
68 ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg 1239
69 Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val
70 175          180          185          190
71 ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc 1287
72 Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly
73          195          200          205
74 tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca 1335
75 Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser
76          210          215          220
77 gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag 1383
78 Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys
79          225          230          235
80 tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata 1431
81 Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile
82          240          245          250
83 aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac 1479
84 Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp
85 255          260          265          270
86 tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac 1527
87 Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp
88          275          280          285
89 tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat 1575
90 Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His
91          290          295          300
92 ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac 1623
93 Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn
94          305          310          315
95 gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg 1671
96 Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg
97          320          325          330
98 gag aca gta ctg tca tct gca tta taacggactg tgatgggac acatgagcaa 1725
99 Glu Thr Val Leu Ser Ser Ala Leu
100 335          340
101 atttttcagct ctcaaaaggca aaggacactc ctttctaatt gcacacctt ctcatcagat 1785
102 tgaataaaaaa aaagcactg aaacccaatt actgaaaaaa aattgacagc tagtggtttt 1845
103 taccatccgt cattacccaa agacttggga actaaaatgt tccccaggt gatatgctga 1905

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104 ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965
105 atacaaatta tgtcttccaa agtatggaac actccaatca gaaaaagggtt atcatcccg 2024
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 547
109 <212> TYPE: PRT
110 <213> ORGANISM: Homo Sapiens
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Deduced Amino Acid Sequence of Novel Collectin from Nucleotide
114 Sequence
116 <400> SEQUENCE: 2
117 Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu
118 1 5 10 15
119 Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val
120 20 25 30
121 Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn
122 35 40 45
123 Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys
124 50 55 60
125 Glu Lys Val Gln Ser Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu
126 65 70 75 80
127 Ala Lys Ala Asn Asn Asp Thr Leu Glu Asp Met Asn Ser Glu Leu Asn
128 85 90 95
129 Ser Phe Thr Gly Gln Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn
130 100 105 110
131 Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn
132 115 120 125
133 Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu Glu Arg Phe Gln Leu Phe
134 130 135 140
135 Glu Thr Asp Ile Val Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His
136 145 150 155 160
137 His Leu Arg Thr Leu Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys
138 165 170 175
139 Thr Asp Thr Leu Thr Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn
140 180 185 190
141 Thr Leu Ala Asn Ile Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln
142 195 200 205
143 Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val
144 210 215 220
145 Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile
146 225 230 235 240
147 Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg
148 245 250 255
149 Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly
150 260 265 270
151 Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu
152 275 280 285
153 Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys
154 290 295 300
155 Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly

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156 305          310          315          320
157 Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro
158          325          330          335
159 Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln
160          340          345          350
161 Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly
162          355          360          365
163 Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro
164          370          375          380
165 Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln
166 385          390          395          400
167 Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly Cys Pro Pro His Trp
168          405          410          415
169 Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile
170          420          425          430
171 Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val
172          435          440          445
173 Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val
174          450          455          460
175 Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn
176 465          470          475          480
177 Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys
178          485          490          495
179 Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro Gly Glu Asp
180          500          505          510
181 Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu
182          515          520          525
183 Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser
184          530          535          540
185 Ser Ala Leu
186 545
188 <210> SEQ ID NO: 3
189 <211> LENGTH: 27
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Modified Consensus Sequence of collectins Hybridizable with Novel
195 Collectin
197 <400> SEQUENCE: 3
198 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn
199 1          5          10          15
200 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe
201          20          25
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 21
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Sequence of a Reverse Primer for Screening a Novel Collectin.

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211 <400> SEQUENCE: 4
212 caatctgatg agaaggtgat g                               21
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 21
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Sequence of a Forward Primer for Screening a Novel Collectin.
222 <400> SEQUENCE: 5
223 acgaggggct g gatgggaca t                               21
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 27
227 <212> TYPE: PRT
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Consensus sequence of three collectins which were reported
232 heretofore
234 <400> SEQUENCE: 6
235 Glu Asp Cys Val Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro
236 1 5 10 15
237 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe
238 20 25
240 <210> SEQ ID NO: 7
241 <211> LENGTH: 24
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: M13 Universal Primer Sequence for Sequencing
248 <400> SEQUENCE: 7
249 cgacgttgta aaacgacggc cagt                               24
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 17
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: M13 Reverse Primer Sequence for Sequencing.
259 <400> SEQUENCE: 8
260 caggaaaca gctatgac                                     17
262 <210> SEQ ID NO: 9
263 <211> LENGTH: 24
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Sequence of a lambda gtl1 Reverse Primer for Sequencing.
270 <400> SEQUENCE: 9
271 ttgacaccag accaactggt aatg                               24
273 <210> SEQ ID NO: 10
274 <211> LENGTH: 24
275 <212> TYPE: DNA

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VERIFICATION SUMMARY DATE: 03/07/2001
PATENT APPLICATION: US/09/763,712 TIME: 13:13:30

Input Set : A:\37157SEQ.txt
Output Set: N:\CRF3\03072001\I763712.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date